#8

PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/09/084,491A

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This Raw Listing contains the General Information Section and up to the first 5 pages.

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ENTERED
                                      SEQUENCE LISTING
 1
 2
    (1)
           General Information:
 4
          (i) APPLICANT: MOORE, PAUL A.
 5
    RUBEN, STEVEN M.
 7
    EBNER, REINHARD
 8
 9
        (ii) TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR-LIKE PROTEASE
10
       (iii) NUMBER OF SEQUENCES: 16
11
12
        (iv) CORRESPONDENCE ADDRESS:
1.3
14
               (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
               (B) STREET: 9410 KEY WEST AVENUE
15
               (C) CITY: ROCKVILLE
16
17
               (D) STATE: MD
               (E) COUNTRY: USA
18
19
               (F) ZIP: 20850
20
21
          (V) COMPUTER READABLE FORM:
               (A) MEDIUM TYPE: Floppy disk
22
               (B) COMPUTER: IBM PC compatible
23
               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24
               (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26
27
         (vi) CURRENT APPLICATION DATA:
28
               (A) APPLICATION NUMBER: 09/084,491
29
               (B) FILING DATE: 27-MAY-1998
               (C) CLASSIFICATION:
30
31
32
      (viii) ATTORNEY/AGENT INFORMATION:
33
               (A) NAME: BROOKES, ANDERS A.
34
               (B) REGISTRATION NUMBER: 36,373
               (C) REFERENCE/DOCKET NUMBER: PF378
35
36
37
         (ix) TELECOMMUNICATION INFORMATION:
38
               (A) TELEPHONE: (301) 309-8504
39.
               (B) TELEFAX: (301) 309-8439
40
41
42
    (2) INFORMATION FOR SEQ ID NO:1:
43
44
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 2329 base pairs
45
               (B) TYPE: nucleic acid
46
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69	TTA	CCAG	AAC A	AGCA'	l'AAC!	AA G	GCA	3G'I'C'	r GA	CTGC	AAGC	TGG	JAC'I'	GGG .	AGGCA	AGAGCC	60
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71	GCCC	3CCA1	AGG (3GGC(CTCG	ST TA	AAACI	ACTG	G TC	3'I''I'C	AATC	ACC.	rgca	AGA (CGAA	GAGGCA	120
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73	AGG														ATG	•	168
74 75			-20	red	Ala	тър	νат	-15	АТа	Pne	rea	νат	-10	ASn	Met	ren	
75 76	ì	-21	-20					-15					-10				
70 77	CITIA	CCA	GAA	aaa	חאח	GGA	ጥረጥ	GGA	aaa	መረመ	መመረባ	ጥርር	GAC	אאמ	GGC	CAC	216
78		_	_	_		_		_	_						Gly		210
79	nea	-5	GIU	AIG	1 7 2	GLY	1	O L y	GLY	cys	5	11.5	АЗР	ASII	GLY	10	
80		J					*				•					10	
81	CTG	ТΔС	CGG	GAG	GAC	CAG	ACC	TCC	CCC	GCG	CCG	GGC	CTC	CGC	TGC	CTC	264
82															Cys		201
83	200	-1-	9	-	15			~~-		20		<u>1</u>	204	5	25	204	
84										20					20		
85	AAC	TGG	CTG	GAC	GCG	CAG	AGC	GGG	CTG	GCC	TCG	GCC	CCC	GTG	TCG	GGG	312
86															Ser		012
87		F		30				- _1	35					40	201	~ <i></i>	
88														- •			
89	GCC	GGC	AAT	CAC	AGT	TAC	TGC	CGA	AAC	CCG	GAC	GAG	GAC	CCG	CGC	GGG	360
90															Arg		
91			45			- 4	4	50			•		55		·· J	.	
92																	
93	CCC	TGG	TGC	TAC	GTC	AGT	GGC	GAG	GCC	GGC	GTC	CCT	GAG	AAA	CGG	CCT	408
94															Arg		_ _ _
95		60	<u>,</u>	. –		_	65					70		3	J		
96												-					
97	TGC	GAG	GAC	CTG	CGC	TGT	CCA	GAG	ACC	ACC	TCC	CAG	GCC	CTG	CCA	GCC	456
98	Cys	Glu	Asp	Leu	Arg	Cys	Pro	Glu	Thr	Thr	Ser	Gln	Ala	Leu	Pro	Ala	
99	75		-			80					85					90	

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101															GAT Asp		504
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104					75					100					103		
105	GTG	CAG	GTG	TTC	GCT	ССТ	GCC	AAC	GCC	CTG	CCC	GCT	CGG	AGT	GAG	GCG	552
106	_	_	_	_			_								Glu		332
107				110					115				9	120			
108														•			
109	GCA	GCT	GTG	CAG	CCA	GTG	ATT	GGG	ATC	AGC	CAG	CGG	GTG	CGG	ATG	AAC	600
110	Ala	Ala	Val	Gln	Pro	Val	Ile	Gly	Ile	Ser	Gln	Arg	Val	Arg	Met	Asn	•
111			125		•			130					135				•
112																	
113	TCC	AAG	GAG	AAA	AAG	GAC	CTG	GGA	ACT	CTG	GGC	TAC	GTG	CTG	GGC	ATT	648
114	Ser	Lys	Glu	Lys	Lys	Asp	Leu	Gly	Thr	Leu	Gly	Tyr	Val	Leu	Gly	Ile	
115		140					145					150					
116																	
117															TTG		696
118	Thr	Met	Met	Val	Ile	Ile	Ile	Ala	Ile	Gly	Ala	Gly	Ile	Ile	Leu	Gly	
119	155					160					165					170	
120						41.											
121															CAG		744
122	Tyr	Ser	Tyr	Lys	_	GTÄ	Lys	Asp	Leu	_	GLU	GIN	His	Asp	Gln	Lys	
123				•	175					180					185		
124	CITE N	mam	a a a	3.00	a s a	N M CI	a. a	aas	» ma	» am	ama	000	mma	mam	aaa	mma	700
125 126															GCC		792
127	vат	Cys	GIU	190	GIU	мес	GTII	Arg	195	1111	rea	PIO	ьeu	200	Ala	Pile	
128				190					193					200			
129	ΔCC	ልልሮ	מממ	ΔCC	ጥርጥ	GAG	אַיייים	GTG	СΔΨ	GAG	AAG	ΣСЩ	ርጥሮ	GTG	GTC	CAC	840
130															Val		040
131		11211	205		0	-		210	p	00			215	741	V G I		
132																	
133																	
134	ACC	AGC	CAG	ACT	CCA	GTT	GAC	CCT	CAG	GAG	GGC	AGC	ACC	CCC	CTT	ATG	888
135	Thr	Ser	Gln	Thr	Pro	Val	Asp	Pro	Gln	Glu	Gly	Ser	Thr	Pro	Leu	Met	
136		220					225				_	230					
137						,											
138	GGC	CAG	GCC	GGG	ACT	CCT	GGG	GCC	T GA	AGCCC	cccc	AG	CGGGC	CAGG			933
139	Gly	Gln	Ala	Gly	Thr	Pro	Gly	Ala									
140	235					240											
141																	
142	AGC	CATO	GCA (GACAC	CTGGT	rg CA	AGGAC	CAGC	CAC	CCTC	CTA	CAG	CTAGO	GAG (GAACT	TACCAC	993
143			-~	~~~								maaa					1052
144	TTTC	3.I.G.I]	rch (3G'I'I'	AAA	ניט טנ	ACCA	ACTCC	e eec	JGC'I''I	l'T'T'T	TGGC	JGAA'I	ree .	l'AGT'	AAGAGT	1053
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146 147	GACE	JAAOr	J A C	O T G(IG T		CAGC	o GTF	MUGU	166	GIAC	JUGT(HUAL	310010	1112
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150	ርኔሞር	<u></u> የርጥር	ነጥር፤ ረ	ነጥል ልጥ	ימניתיי	פייי פי	!ልልልሰ	<u>ነ</u> ልጥጥረ	ן הרח	יממאר	ימממ	ጥ ርር ፣	<u>አ</u> ለ ር ጥር	300	<u> </u>	GATAG	1233
151	OAIC			~ * *3***/			- 4 4 5 3 A 3 \	A L C		COAC		1001				JAIAU	1233
	ACGO	GGAC	CT (cccc	CAGGO	CT CC	СТСТС	STGCT	יייי <i>י</i> יי	CTA	GAT	GGCT	CAGT	CT (CCACT	TGTGGG	1293
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153 154	CTTGAGTGGC	ATACACTGTT	ATTCATGGTT	AAGGTAAAGC	AGGTCAAGGG	ATGGCATTGA	1353
155							
156 157	AAAAATATAT	TTAGTTTTTA	AAATATTTGG	GATGGAACTC	CCTACTGACC	TCTGACAACT	1413
158 159	GGAAACGAGT	TTGTACTGAA	GTCAGAACTT	TGGGTTGGGA	ATGAGATCTA	GGTTGTGGCT	1473
160 161	GCTGGTATGC	TTCAGCTTGC	TGGCAATGAT	GTGCCTTGAC	AACCGTGGGC	CAGGCCTGGG	1533
162 163	CCCAGGGACT	CTTCCTGTTT	CATAAGGAAA	GGAAGAATTG	CACTGAGCAT	TCCACTTAGG	1593
164	AAGAGGATAG	AGAAGGATCT	GCTCCGCCTT	TGGCCACAGG	AGCAGAGGCA	GACCTGGGAT	1653
165 166	GCCCCAGTTT	CTCTTCAGGG	ATGGATAGTG	ACCTGTCTTC	ATTTTGCACA	GGTAAGAGAG	1713
167 168	TAGTTAGCTA	ACCTATGGGA	ATTATACTGT	GGGCCTTGT	GAGCTGCTTC	TAAGAGGCTA	1773
169 170	ACCTGGAAAC	TAAGCTCAGA	GGCAAGGTAA	TAAAGCACTT	CAGGGCTTGC	TCCCCAAGTG	1833
171 172	GGCCTGATTT	AGCAGGTGGT	CTGCGGGCGT	CCAGGTCAGC	ACCTTCCTGT	AGGGCACTGG	1893
173 174	GGCTAGGGTC	ACAGCCCCTA	ACTCATAAAG	CAATCAAAGA	ACCATTAGAA	AGGGCTCATT	1953
175 176	AAGCCTTTTG	GACACAGGAC	CCCAGAGAGG	AAAAAGTGA C		TCGTAAGCAA	2013
177 178	GCTACTGGCA	TGGCAAGAGC	CCAGCTTCCT	GACGGAGCGC	AACATTTCTC	CACTGCACTG	2073
179 180	TGCTAGCAGC	TCAGCAGGGC	CTCTAACCTG	TGATGTCACA	CTCAAGAGGC	CTTGGCAGCT	2133
181 182	CCTAGCCATA	GAGCTTCCTT	TCCAGAACCC	TTCCACTGCC	CAATGTGGAG	ACAGGGGTTA	2193
183 184	GTGGGGCTTT	CTATGGAGCC	ATCTGCTTTG	GGGACCTAGA	CCTCAGGTGG	TCTCTTGGTG	2253
185 186	TTAGTGATGC	TGGAGAAGAG	AATATTACTG	GTTTCTACTT	TTCTATAAAG	GCATTTCTCT	2313
187	л шлллллллл					•	2220
188 189	АТААААААА	AAAAA					2329
190							
191	(2) INFORM	ATION FOR SI	EQ ID NO:2:				
192 193	/ i \	SEQUENCE CH	JADA∕MEDT¢M¹	rag.			
194	(1)		TH: 263 amin				
195		• •	amino acio				
196		` '	LOGY: linear				
197		(= / = = = =		-			
198	(ii)	MOLECULE TY	PE: protein	n		·	
199	•						
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201	(xi)	SEQUENCE DE	ESCRIPTION:	SEQ ID NO:2	2:		
202	Wot Fam Fam	, ala m ''	.1 (1)1 - •	7ha Fan 17-7	Com Nam Mad	. Tou Tou	
203 204	Met Leu Leu	ı Ala Trp Va	al Gin Ala P -15	ue ren var	Ser Asn Met	r ren ren	
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206 . 207	Ala -5	Glu	Ala	Tyr	Gly	_	Gly	Gly	Cys	Phe 5	Trp	Asp	Asn	Gly	His 10	Leu
207	-3					1				5						
209	Пттт	λrα	Glu	λen	Cln	mb ~	Sor	Dro	λla	Dro	G] 17	T 011	h ra	Cuc	Len	N an
210	ıyı	ALG	GIU	15	GTII	1111	Ser	PIO	20	PIO	сту	ьеu	Arg	25	пец	ASII
211				13					20					23		
212	mr»	T 011	Asp	λΙο	Cln	802	C1 11	T 011	בוג	Sar	λla	Dro	บาไ	Sor	C1 17	מ 1 ג
	пр	Leu	30	Ата	GTII	261	GTA	35	мта	Ser	АТА	PIO	40	ser	сту	АТА
213			30					33					40			
214	al	3 ~ ~	TT 4 ~	C0 m	Messo	7	7 w ~	A a m	Dwo	7 ~~	a 1	7 an	Dwo	X = ~	~1	Dro
215	GTA		His	Ser	TYL	Cys	_	ASII	PIO	ASP	GIU	_	PIO	Arg	стА	PIO
216		45					50					55				
217	(II)	0	M	Wa I	C	al	~1	3 T o	a 1	1703	Dwo	a 1	T	1	Dwo	0
218	-	Cys	Tyr	val	Ser	-	GIU	АТЯ	сту	vaı		GIU	гуѕ	Arg	Pro	-
219	60					65					70					75
220	a 1	3	T	3	a	D	a 1	mb	mb	G	~ 1	37 a	T	Desc	77-	Dha
221	GIU	Asp	Leu	Arg	-	Pro	GIU	THE	THE		GIN	Ата	ьеи	Pro		Pne
222					80					85					90	
223	ml	mb	a 1	-1 -	a 1	a 1		a'	a 3	a 1	D=0	ai	. 77 ~	3	~1	17.3
224 ~	Thr	Thr	Glu		GIN	GIU	ATA	Ser		GTA	Pro	GTA	АТа	_	GIU	vaı
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227			Phe									_		GIU	АТа	Ala
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229		•• - 7	~ 1	5	••- 7	-1 -	43	- 1.	~	a 1	3	**- 3	3	M -4	1	a
230	ATa		Gln	Pro	val	TT6	-	тте	ser	GIN	Arg		Arg	мет	Asn	Ser
231		125					130					135				
232	_	~ 3	_	_	_	_		_1	_	~ 3	_	7	_	~ T		-1
233	_	GLu	Lys	Lys	Asp		СТÅ	Thr	Leu	GTA	_	Val	Leu	GTA	TTE	
234	140					145					150					155
235									- 9		~ 3			_	 7	
236	Met	Met	Val	IIe		IIe	Ala	Ile	GTA	•	СΤÄ	Ile	ITe	Leu	_	Tyr
237					160					165					170	
238		_	_		3	_		_	_	~7	~ 7	'		~3	_	7
239	Ser	Tyr	Lys	_	СТА	Lys	Asp	Leu	_	GLU	GIN	Hls	Asp		Lys	Val
240				175					180					185		
241	_	~ 3	_	P	1				-1	_	_	_	~	- 1	~1 .	-1
242	Cys	GIu	Arg	GLu	Met	GIn	Arg		Thr	Leu	Pro	Leu		Ala	Pne	Thr
243			190					195					200			
244	_									_	_,				'	_1
245	Asn		Thr	Cys	GIu	IIe		Asp	GLU	Lys	Thr		val	vaı	HIS	Thr
246		205					210					215				
247				_						7		_,	_	_		
248		GLn	Thr	Pro	Val	-	Pro	GIn	GLu	GTÀ		Thr	Pro	Leu	Met	_
249	220					225					230					235
250						_	_									
251	Gln	Ala	Gly	Thr		Gly	Ala								,	
252					240											
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254	(2)	INF	ORMAT	MOI	FOR	SEQ	ID 1	10:3:	•							
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256		(i)) SE(QUENC	CE CH	IARAC	TER]	STIC	CS:							
257			•	•	ENGTH				acid	ds						
258			(E	3) TS	PE:	amir	no ac	cid								

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